

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ashkenazi et al.
- (ii) TITLE OF INVENTION: RTD Receptor
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: Genentech, Inc.
 (B) STREET: 1 DNA Way
 (C) CITY: South San Francisco
 (D) STATE: California
 (E) COUNTRY: USA
 (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER:
 (B) FILING DATE:
 (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Marschang, Diane L.
 (B) REGISTRATION NUMBER: 35,600
 (C) REFERENCE/DOCKET NUMBER: P1129
- (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: 650/225-5416
 (B) TELEFAX: 650/952-9881
- (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 386 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Gly	Leu	Trp	Gly	Gln	Ser	Val	Pro	Thr	Ala	Ser	Ser	Ala	Arg
1				5					10					15
Ala	Gly	Arg	Tyr	Pro	Gly	Ala	Arg	Thr	Ala	Ser	Gly	Thr	Arg	Pro
				20					25					30

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4232044881590

	Trp	Leu	Leu	Asp	Pro	Lys	Ile	Leu	Lys	Phe	Val	Val	Phe	Ile	Val
					35					40					45
5	Ala	Val	Leu	Leu	Pro	Val	Arg	Val	Asp	Ser	Ala	Thr	Ile	Pro	Arg
					50					55					60
	Gln	Asp	Glu	Val	Pro	Gln	Gln	Thr	Val	Ala	Pro	Gln	Gln	Gln	Arg
					65					70					75
10	Arg	Ser	Leu	Lys	Glu	Glu	Glu	Cys	Pro	Ala	Gly	Ser	His	Arg	Ser
					80					85					90
	Glu	Tyr	Thr	Gly	Ala	Cys	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	Tyr
					95					100					105
15	Thr	Ile	Ala	Ser	Asn	Asn	Leu	Pro	Ser	Cys	Leu	Leu	Cys	Thr	Val
					110					115					120
	Cys	Lys	Ser	Gly	Gln	Thr	Asn	Lys	Ser	Ser	Cys	Thr	Thr	Thr	Arg
20					125					130					135
	Asp	Thr	Val	Cys	Gln	Cys	Glu	Lys	Gly	Ser	Phe	Gln	Asp	Lys	Asn
					140					145					150
25	Ser	Pro	Glu	Met	Cys	Arg	Thr	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly
					155					160					165
	Met	Val	Lys	Val	Ser	Asn	Cys	Thr	Pro	Arg	Ser	Asp	Ile	Lys	Cys
30					170					175					180
	Lys	Asn	Glu	Ser	Ala	Ala	Ser	Ser	Thr	Gly	Lys	Thr	Pro	Ala	Ala
					185					190					195
35	Glu	Glu	Thr	Val	Thr	Thr	Ile	Leu	Gly	Met	Leu	Ala	Ser	Pro	Tyr
					200					205					210
	His	Tyr	Leu	Ile	Ile	Ile	Val	Val	Leu	Val	Ile	Ile	Leu	Ala	Val
					215					220					225
40	Val	Val	Val	Gly	Phe	Ser	Cys	Arg	Lys	Lys	Phe	Ile	Ser	Tyr	Leu
					230					235					240
	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Gly	Pro	Glu	Arg	Val	His
45					245					250					255
	Arg	Val	Leu	Phe	Arg	Arg	Arg	Ser	Cys	Pro	Ser	Arg	Val	Pro	Gly
					260					265					270
50	Ala	Glu	Asp	Asn	Ala	Arg	Asn	Glu	Thr	Leu	Ser	Asn	Arg	Tyr	Leu
					275					280					285
	Gln	Pro	Thr	Gln	Val	Ser	Glu	Gln	Glu	Ile	Gln	Gly	Gln	Glu	Leu

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269230-12881680

					290					295					300
	Ala	Glu	Leu	Thr	Gly	Val	Thr	Val	Glu	Xaa	Pro	Glu	Glu	Pro	Gln
					305					310					315
5	Arg	Leu	Leu	Glu	Gln	Ala	Glu	Ala	Glu	Gly	Cys	Gln	Arg	Arg	Arg
					320					325					330
10	Leu	Leu	Val	Pro	Val	Asn	Asp	Ala	Asp	Ser	Ala	Asp	Ile	Ser	Thr
					335					340					345
	Leu	Leu	Asp	Ala	Ser	Ala	Thr	Leu	Glu	Glu	Gly	His	Ala	Lys	Glu
					350					355					360
15	Thr	Ile	Gln	Asp	Gln	Leu	Val	Gly	Ser	Glu	Lys	Leu	Phe	Tyr	Glu
					365					370					375
	Glu	Asp	Glu	Ala	Gly	Ser	Ala	Thr	Ser	Cys	Leu				
					380					385	386				

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	CCA	ACT	GC	CAC	CTC	GTT	CTA	TCG	ATT	GA	AAT	TCCC	CG	GG	GGA	TC	CT	TA	GAG	50			
	AT	CC	CT	CG	AC	CC	CAC	GCG	TCC	GG	AA	CCT	TT	GC	CAC	CG	CG	CA	AA	ACT	100		
	AC	GG	GG	AC	GA	TTT	CT	GAT	TG	AT	TTT	TG	GC	G	CT	TC	GAT	CC	ACC	CT	CT	CC	150
	CT	TCT	C	ATG	GGA	CTT	TGG	GGA	CAA	AGC	GTC	CCG	ACC	GCC						189			
40				Met	Gly	Leu	Trp	Gly	Gln	Ser	Val	Pro	Thr	Ala									
				1				5					10										
	TCG	AGC	GCT	CGA	GCA	GGG	CGC	TAT	CCA	GGA	GCC	AGG	ACA							228			
	Ser	Ser	Ala	Arg	Ala	Gly	Arg	Tyr	Pro	Gly	Ala	Arg	Thr										
				15					20														
45	GCG	TCG	GGA	ACC	AGA	CCA	TGG	CTC	CTG	GAC	CCC	AAG	ATC							267			
	Ala	Ser	Gly	Thr	Arg	Pro	Trp	Leu	Leu	Asp	Pro	Lys	Ile										
	25					30					35												
50	CTT	AAG	TTC	GTC	GTC	TTC	ATC	GTC	GCG	GTT	CTG	CTG	CCG							306			
	Leu	Lys	Phe	Val	Val	Phe	Ile	Val	Ala	Val	Leu	Leu	Pro										
				40				45					50										

	GTC	CGG	GTT	GAC	TCT	GCC	ACC	ATC	CCC	CGG	CAG	GAC	GAA	345
	Val	Arg	Val	Asp	Ser	Ala	Thr	Ile	Pro	Arg	Gln	Asp	Glu	
					55					60				
5	GTT	CCC	CAG	CAG	ACA	GTG	GCC	CCA	CAG	CAA	CAG	AGG	CGC	384
	Val	Pro	Gln	Gln	Thr	Val	Ala	Pro	Gln	Gln	Gln	Arg	Arg	
		65					70					75		
10	AGC	CTC	AAG	GAG	GAG	GAG	TGT	CCA	GCA	GGA	TCT	CAT	AGA	423
	Ser	Leu	Lys	Glu	Glu	Glu	Cys	Pro	Ala	Gly	Ser	His	Arg	
				80					85					
15	TCA	GAA	TAT	ACT	GGA	GCC	TGT	AAC	CCG	TGC	ACA	GAG	GGT	462
	Ser	Glu	Tyr	Thr	Gly	Ala	Cys	Asn	Pro	Cys	Thr	Glu	Gly	
	90					95					100			
20	GTG	GAT	TAC	ACC	ATT	GCT	TCC	AAC	AAT	TTG	CCT	TCT	TGC	501
	Val	Asp	Tyr	Thr	Ile	Ala	Ser	Asn	Asn	Leu	Pro	Ser	Cys	
			105					110					115	
25	CTG	CTA	TGT	ACA	GTT	TGT	AAA	TCA	GGT	CAA	ACA	AAT	AAA	540
	Leu	Leu	Cys	Thr	Val	Cys	Lys	Ser	Gly	Gln	Thr	Asn	Lys	
					120					125				
30	AGT	TCC	TGT	ACC	ACG	ACC	AGA	GAC	ACC	GTG	TGT	CAG	TGT	579
	Ser	Ser	Cys	Thr	Thr	Thr	Arg	Asp	Thr	Val	Cys	Gln	Cys	
			130				135					140		
35	GAA	AAA	GGA	AGC	TTC	CAG	GAT	AAA	AAC	TCC	CCT	GAG	ATG	618
	Glu	Lys	Gly	Ser	Phe	Gln	Asp	Lys	Asn	Ser	Pro	Glu	Met	
				145					150					
40	TGC	CGG	ACG	TGT	AGA	ACA	GGG	TGT	CCC	AGA	GGG	ATG	GTC	657
	Cys	Arg	Thr	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val	
	155					160					165			
45	AAG	GTC	AGT	AAT	TGT	ACG	CCC	CGG	AGT	GAC	ATC	AAG	TGC	696
	Lys	Val	Ser	Asn	Cys	Thr	Pro	Arg	Ser	Asp	Ile	Lys	Cys	
			170					175					180	
50	AAA	AAT	GAA	TCA	GCT	GCC	AGT	TCC	ACT	GGG	AAA	ACC	CCA	735
	Lys	Asn	Glu	Ser	Ala	Ala	Ser	Ser	Thr	Gly	Lys	Thr	Pro	
					185					190				
55	GCA	GCG	GAG	GAG	ACA	GTG	ACC	ACC	ATC	CTG	GGG	ATG	CTT	774
	Ala	Ala	Glu	Glu	Thr	Val	Thr	Thr	Ile	Leu	Gly	Met	Leu	
		195					200					205		
60	GCC	TCT	CCC	TAT	CAC	TAC	CTT	ATC	ATC	ATA	GTG	GTT	TTA	813
	Ala	Ser	Pro	Tyr	His	Tyr	Leu	Ile	Ile	Ile	Val	Val	Leu	
				210					215					

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	GTC	ATC	ATT	TTA	GCT	GTG	GTT	GTG	GTT	GGC	TTT	TCA	TGT	852
	Val	Ile	Ile	Leu	Ala	Val	Val	Val	Val	Gly	Phe	Ser	Cys	
	220					225					230			
5	CGG	AAG	AAA	TTC	ATT	TCT	TAC	CTC	AAA	GGC	ATC	TGC	TCA	891
	Arg	Lys	Lys	Phe	Ile	Ser	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	
			235					240					245	
10	GGT	GGT	GGA	GGA	GGT	CCC	GAA	CGT	GTG	CAC	AGA	GTC	CTT	930
	Gly	Gly	Gly	Gly	Gly	Pro	Glu	Arg	Val	His	Arg	Val	Leu	
					250					255				
15	TTC	CGG	CGG	CGT	TCA	TGT	CCT	TCA	CGA	GTT	CCT	GGG	GCG	969
	Phe	Arg	Arg	Arg	Ser	Cys	Pro	Ser	Arg	Val	Pro	Gly	Ala	
		260					265					270		
20	GAG	GAC	AAT	GCC	CGC	AAC	GAG	ACC	CTG	AGT	AAC	AGA	TAC	1008
	Glu	Asp	Asn	Ala	Arg	Asn	Glu	Thr	Leu	Ser	Asn	Arg	Tyr	
				275					280					
25	TTG	CAG	CCC	ACC	CAG	GTC	TCT	GAG	CAG	GAA	ATC	CAA	GGT	1047
	Leu	Gln	Pro	Thr	Gln	Val	Ser	Glu	Gln	Glu	Ile	Gln	Gly	
	285					290					295			
30	CAG	GAG	CTG	GCA	GAG	CTA	ACA	GGT	GTG	ACT	GTA	GAG	TYG	1086
	Gln	Glu	Leu	Ala	Glu	Leu	Thr	Gly	Val	Thr	Val	Glu	Xaa	
			300					305					310	
35	CCA	GAG	GAG	CCA	CAG	CGT	CTG	CTG	GAA	CAG	GCA	GAA	GCT	1125
	Pro	Glu	Glu	Pro	Gln	Arg	Leu	Leu	Glu	Gln	Ala	Glu	Ala	
					315					320				
40	GAA	GGG	TGT	CAG	AGG	AGG	AGG	CTG	CTG	GTT	CCA	GTG	AAT	1164
	Glu	Gly	Cys	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Val	Asn	
		325				330						335		
45	GAC	GCT	GAC	TCC	GCT	GAC	ATC	AGC	ACC	TTG	CTG	GAT	GCC	1203
	Asp	Ala	Asp	Ser	Ala	Asp	Ile	Ser	Thr	Leu	Leu	Asp	Ala	
				340					345					
50	TCG	GCA	ACA	CTG	GAA	GAA	GGA	CAT	GCA	AAG	GAA	ACA	ATT	1242
	Ser	Ala	Thr	Leu	Glu	Glu	Gly	His	Ala	Lys	Glu	Thr	Ile	
	350					355					360			
55	CAG	GAC	CAA	CTG	GTG	GGC	TCC	GAA	AAG	CTC	TTT	TAT	GAA	1281
	Gln	Asp	Gln	Leu	Val	Gly	Ser	Glu	Lys	Leu	Phe	Tyr	Glu	
			365					370					375	
60	GAA	GAT	GAG	GCA	GGC	TCT	GCT	ACG	TCC	TGC	CTG	TGAAAG	1320	
	Glu	Asp	Glu	Ala	Gly	Ser	Ala	Thr	Ser	Cys	Leu			
					380					385	386			

AATCTCTTCA GGAAACCAGA GCTTCCCTCA TTTACCTTTT CTCCTACAAA 1370
 GGGAAGCAGC CTGGAAGAAA CAGTCCAGTA CTTGACCCAT GCCCCAACAA 1420
 5 ACTCTACTAT CCAATATGGG GCAGCTTACC AATGGTCCTA GAACTTTGTT 1470
 AACGCACTTG GAGTAATTTT TATGAAATAC TGC GTGTGAT AAGCAAACGG 1520
 GAGAAATTTA TATCAGATTC TTGGCTGCAT AGTTATACGA TTGTGTATTA 1570
 10 AGGGTCGTTT TAGGCCACAT GCGGTGGCTC ATGCCTGTAA TCCCAGCACT 1620
 TTGATAGGCT GAGGCAGGTG GATTGCTTGA GCTCGGGAGT TTGAGACCAG 1670
 15 CCTCATCAAC ACAGTGAAAC TCCATCTCAA TTTAAAAAGA AAAAAAGTGG 1720
 TTTTAGGATG TCATTCTTTG CAGTTCTTCA TCATGAGACA AGTCTTTTTT 1770
 TCTGCTTCTT ATATTGCAAG CTCCATCTCT ACTGGTGTGT GCATTTAATG 1820
 20 ACATCTAACT ACAGATGCCG CACAGCCACA ATGCTTTGCC TTATAGTTTT 1870
 TTAAC TTTAG AACGGGATTA TCTTGTTATT ACCTGTATTT TCAGTTTCGG 1920
 25 ATATTTTTGA CTTAATGATG AGATTATCAA GACGTACCCC TATGCTAAGT 1970
 CATGAGCATA TGGACTTACG AGGGTTCGAC TTAGAGTTTT GAGCTTTAAG 2020
 30 ATAGGATTAT TGGGGGCTTA CCCCACCTT AATTAGAAGA AACATTTTAT 2070
 ATTGCTTTAC TA 2082

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATAAAAGTT CCTGCACCAT GACCAGAGAC ACAGTGTGTC AGTGTAAGA 50

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTTCAGGAAA CCAGAGCTTC CCTC 24

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTCTCCCGTT TGCTTATCAC ACGC 24